

SEQUENCE LISTING

<110> Asundi, Vinod
 Ford, John E.
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 Tang, Y. Tom
 Yamasaki, Vicky
 Yeung, George
 Zhang, Jie
 Zhou, Ping
 Zhou, Hua

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/37665

<150> US 09/687,860

<151> 2000-10-13

<150> US 09/620,312

<151> 2000-07-19

<150> US 09/363,316

<151> 1999-07-28

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Gly Trp Arg	Arg Asn Ser Lys Gly Val	Cys Glu Ala Thr Cys Glu Pro	
1	5	10 15	
gga tgt aag	ttt ggt gag tgc gtg gga cca	aac aaa tgc aga tgc ttt	96
Gly Cys Lys	Phe Gly Glu Cys Val Gly Pro	Asn Lys Cys Arg Cys Phe	
	20	25 30	
cca gga tac	acc ggg aaa acc tgc agt	caa gat gtg aat gag tgt gga	144
Pro Gly Tyr	Thr Gly Lys Thr Cys Ser	Gln Asp Val Asn Glu Cys Gly	
	35	40 45	
atg aaa ccc	cgg cca tgc caa cac aga	tgt gtg aat aca cac gga agc	192
Met Lys Pro	Arg Pro Cys Gln His Arg	Cys Val Asn Thr His Gly Ser	
	50	55 60	
tac aag tgc	ttt tgc ctc agt ggc cac	atg ctc atg cca gat gct acg	240
Tyr Lys Cys	Phe Cys Leu Ser Gly His	Met Leu Met Pro Asp Ala Thr	
65	70	75 80	

28110-37665

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
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gaa	gac	aca	gaa													300
Glu	Asp	Thr	Glu													
			100													

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Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	
1				5					10					15		

gga	tgt	aag	ttt	ggt	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	96
Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	
			20					25					30			

cca	gga	tac	acc	ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	144
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	
		35					40					45				

atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	192
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	
	50					55					60					

tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		

gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	336
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	
			100					105					110			

cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	384
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	
		115					120					125				

tct	ggt	aaa	gtc	atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	432
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
	130					135					140					

gga	agc	tac	tac	tgc	aaa	tgt	cac	att	ggt	ttc	gaa	ctg	caa	tat	atc	480
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	
145					150					155					160	

00001549 101500

agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc	528
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser	
165 170 175	
cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
180 185 190	
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
195 200 205	
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
210 215 220	
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
225 230 235 240	
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
245 250 255	
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
260 265 270	
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
275 280 285	
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
290 295 300	
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
305 310 315 320	
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
325 330 335	
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
340 345 350	
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe	
355 360 365	
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca	1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala	
370 375 380	
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt	1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu	
385 390 395 400	
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat	1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp	
405 410 415	

tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa 1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
420 425 430

aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa 1344
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
435 440 445

aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc 1392
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
450 455 460

aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
465 470 475 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
485 490 495

ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg 1536
Leu Leu Ser Val Xaa Xaa
500

tatgtcagtt ccttggtttt tttgatattg catcatagga cctctggcat tttaaaatta 1596
ctagctgaaa aattg 1611

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<213> Homo sapiens

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Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
50 55 60
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
65 70 75 80
Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
85 90 95
Glu Asp Thr Glu
100

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005440500

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			20					25					30				
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly		
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Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser		
	50					55					60						
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr		
65					70					75					80		
Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys		
			85						90					95			
Glu	Asp	Thr	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Ser	Gly	Leu		
			100					105					110				
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala		
		115					120					125					
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		
	130					135					140						
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile		
145					150					155					160		
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser		
				165					170					175			
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe		
			180					185					190				
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser		
		195					200					205					
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr		
		210				215					220						
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys		
225					230					235					240		
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro		
			245						250					255			
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser		
			260					265					270				
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met		
		275				280					285						
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn		
		290				295					300						
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val		
305					310					315					320		
Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu		
			325							330				335			
Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser		
			340					345					350				
Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe		
		355					360					365					
Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala		
		370				375					380						
Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu		
					390					395					400		
Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp		
			405						410					415			
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys		
			420					425					430				
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu		
		435					440					445					
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr		
		450				455					460						
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu		
					470					475					480		
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser		
				485					490					495			
Leu	Leu	Ser	Val	Asp	Asp	Xaa	Met	Val	Leu	Ser	Leu	Tyr	Leu	Thr	Leu		
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515 520 525

Ile Leu Lys Leu Leu Ala Glu Lys Leu
530 535

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ggaggc	ggcg	gcttag	ctgc	tacggg	gtcc	ggccgg	cgcc	ctccc	gaggg	gggtc	cagga		180			
ggagga	aagga	ggaccc	gtgc	gaga	atg	cct	ctg	ccc	tgg	agc	ctt	gcg	ctc	231		
				Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu				
				1				5								
ccg	ctg	ctg	ctc	ccc	tgg	gtg	gca	ggg	ggg	tac	ggg	aac	gcg	gcc	agt	279
Pro	Leu	Leu	Leu	Pro	Trp	Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	
10					15					20					25	
gca	agg	cat	cac	ggg	ttg	tta	gca	tcg	gca	cgt	cag	cct	ggg	gtc	tgt	327
Ala	Arg	His	His	Gly	Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	
				30					35					40		
cac	tat	gga	act	aaa	ctg	gcc	tgc	tgc	tac	ggc	tgg	aga	aga	aac	agc	375
His	Tyr	Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	
			45					50						55		
aag	gga	gtc	tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	ggg	gag	423
Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	
		60					65					70				
tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	471
Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	
	75					80					85					
acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	519
Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
	90					95				100					105	
caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	567
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	
				110					115					120		
agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	615
Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	
			125					130					135			
tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	gaa	gac	aca	gaa	gaa	ggg	663
Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	
		140					145					150				
cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	711
Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	
	155						160				165					

aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	

00001649-101501

cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt 1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly
430 435 440

cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa 1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln
445 450 455

ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac 1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp
460 465 470

aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg 1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu
475 480 485

gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa 1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys
490 495 500 505

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa 1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu
510 515 520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc 1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val
525 530 535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
540 545 550

tga atgttactat ctttatatatt gactttgtat gtcagttccc tgggttttttt 1916
*

gatattgsat cataggacct ctggcatttt aaaattacta agctgaaaaa ttgtaatgta 1976
ccaacagaaa ttattattgt aagatgcctt tmttgataaa gatatgccaa tatttgcttt 2036
aaatatcata tcactgtatc ttctcagtc tttctgaatc tttccacatt atattataaa 2096
atatggaaat gtcaggttta tctccctcc tcagtatatc tgatttgtat aagtaagttg 2156
atgagcttct cctgcaaca tttctagaaa atagahaaaa aagcacagag aaatgtttta 2216
ctgtttgact cttatgatag tttttggaaa ctatgacatc aaagatagac ttttgcctaa 2276
gtggcttagc tgggtctttc atagccaaac ttgtatatatt aaattctttg taataataat 2336
atccaaatca tcaaaaaaaa aaaaaaaaaa 2365

<210> 6
<211> 553
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(553)
<223> Xaa = Any Amino Acid

<400> 6
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Pro Trp Val
1 5 10 15
Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly Leu Leu
20 25 30
Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
35 40 45

00001519 101501

Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
	50					55					60				
Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
65				70					75					80	
Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
				85					90					95	
Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
			100					105					110		
His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
		115					120					125			
Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln
	130					135					140				
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145				150						155				160	
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
				165					170					175	
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
			180					185					190		
Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu
		195					200					205			
Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr
	210					215					220				
Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln
225				230						235				240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu
			245						250					255	
Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
			260					265					270		
Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn
		275					280					285			
Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr
	290					295					300				
Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu
305				310						315				320	
Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu
				325					330					335	
Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala
			340					345					350		
Leu	Lys	Asn	Asp	Xaa	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe
		355					360					365			
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg
	370					375					380				
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val
385				390						395				400	
Asp	Cys	Ser	Phe	Asn	His	Gly	Ile								

Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

<210> 7
<211> 42
<212> PRT
<213> Drosophila Melanogaster

<220>
<221> VARIANT
<222> (1)...(42)
<223> Xaa = Any Amino Acid

<400> 7
Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa
1 5 10 15
Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
20 25 30
Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
35 40

<210> 8
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(39)
<223> Xaa = Any Amino Acid

<400> 8
Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
1 5 10 15
Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa
20 25 30
Gly Xaa Xaa Leu Xaa Cys Asp
35

<210> 9
<211> 164
<212> PRT
<213> Homo sapiens

<400> 9
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Val Asn
1 5 10 15
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
20 25 30
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
35 40 45
Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
50 55 60
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
65 70 75 80
Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
85 90 95
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
100 105 110
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
115 120 125
Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn
130 135 140

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Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
 145 150 155 160
 Leu Arg Cys Ser

<210> 10
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(45)
 <223> Xaa = Any Amino Acid

<400> 10
 Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa
 1 5 10 15
 Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly
 20 25 30
 Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp
 35 40 45

<210> 11
 <211> 58
 <212> PRT
 <213> Mammalian

<220>
 <221> VARIANT
 <222> (1)...(58)
 <223> Xaa = Any Amino Acid

<400> 11
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 1 5 10 15
 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 20 25 30
 Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln
 35 40 45
 Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
 50 55

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-52

<400> 12
 ctcacacctca agccctctt t

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-51

<400> 13

ccatgagagt tcccgcctct g 21

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer T7

<400> 14
gtaatacgac tcactatagg g 21

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer SP6

<400> 15
atttaggtga cactatagaa gg 22

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-A

<400> 16
cccaggctga cgtgccgatg c 21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-B

<400> 17
gcagcaggcc agtttagttc c 21

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(502)
<223> Xaa = Any Amino Acid

<400> 18
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
1 5 10 15
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45

1053101 54373662

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<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: primer

<400> 19

gtcattttctg aatcttttcca c

21

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

gaaatgttgc agagagaagc tc

22

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 21

ccagaaccca ccaggactcc

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

gggaactgac atacaaagtc

<210> 23

<211> 2365

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (205)..(1863)

<400> 23

actagtgtatt ccataccta acgactcact atagggctcg agcggccgcc cgggcaggtc 60

tgcagggaca gcacccggta actgcgagtg gagcggagga cccgagcggc tgaggagaga 120

ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccgaggg gggctcagga 180

ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc 231

Met Pro Leu Pro Trp Ser Leu Ala Leu

1

5

ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279

Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser

10

15

20

25

gca agg cat cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt	327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys	
30 35 40	
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc	375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser	
45 50 55	
aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	

00001649 101501

aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac	1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp	
460 465 470	
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg	1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu	
475 480 485	
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa	1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys	
490 495 500 505	
att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa	1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu	
510 515 520	
gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc	1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val	
525 530 535	

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ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863
 Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
 540 545 550

tgaatgttac tatctttata tttagactttg tatgtcagtt ccctggtttt tttagatattg 1923
 satcatagga cctctggcat tttaaaatta ctaagctgaa aaattgtaat gtaccaacag 1983
 aaattattat tgtaagatgc ctttmttgta taagatatgc caatatttgc tttaaatatc 2043
 atatcactgt atcttctcag tcattttctga atctttccac attatattat aaaatatgga 2103
 aatgtcaggt ttatctcccc tcctcagtat atctgatttg tataagtaag ttgatgagct 2163
 tctctctgca acattttctag aaaatagaha aaaaagcaca gagaaatgtt taactgtttg 2223
 actcttatga tagtttttgg aaactatgac atcaaagata gacttttgcc taagtggctt 2283
 agctgggtct ttcataagcca aacttgata tttaaattct ttgtaataat aatatccaaa 2343
 tcatcaaaaa aaaaaaaaaa aa 2365

<210> 24
 <211> 553
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(553)

<400> 24

Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp Val
 1 5 10 15
 Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly Leu Leu
 20 25 30
 Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
 35 40 45
 Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
 50 55 60
 Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
 65 70 75 80
 Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
 85 90 95
 Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
 100 105 110
 His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
 115 120 125
 Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
 130 135 140
 Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
 145 150 155 160

Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
165 170 175

Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
210 215 220

Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn
275 280 285

Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
340 345 350

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe
355 360 365

Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg
370 375 380

Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val
385 390 395 400

Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu
405 410 415

Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe
420 425 430

Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg
435 440 445

Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu
450 455 460

Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val
465 470 475 480

Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser
485 490 495

00001649-101501

Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr
500 505 510

Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys
515 520 525

Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys
530 535 540

Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ccctggcatg ggagaagacc ac 22

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gtgatatgat atttaaagca aatattggca 30

<210> 27
<211> 2360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (190)..(1869)

<220>
<221> misc_feature
<222> (1)...(2360)
<223> n = a,t,c or g

<400> 27
cctctatatg catgctcgag cgcggncgca gtgtgatgga tatctgcaga attcggctta 60

ctcactatag ggctcgagcg gccgcccggg caggtgagga gagaggaggc ggcggcttag 120

ctgctacggg gtccgggccg gcgccctccc gaggggggct caggaggagg aaggaggacc 180

cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
1 5 10

tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct	276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser	
14 19 24 29	
cat cat cat cat cat cac ggg ttg tta gca tgc gca cgt cag cct ggg	324
His His His His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly	
30 35 40 45	
gtc tgt cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga	372
Val Cys His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg	
46 51 56 61	
aac agc aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt	420
Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe	
62 67 72 77	
ggg gag tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc	468
Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr	
78 83 88 93	
ggg aaa acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg	516
Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg	
94 99 104 109	
cca tgc caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt	564
Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe	
110 115 120 125	
tgc ctc agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct	612
Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser	
126 131 136 141	
agg aca tgt gcc atg ata aac tgt cag tac agc tgt gaa gac aca gaa	660
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu	
142 147 152 157	
gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca	708
Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro	
158 163 168 173	
aat gga aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc	756
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Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg	
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 Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln
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Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala
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 Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys
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 Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val
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 Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn
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 Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile
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Val	Asp	Cys	Ser	Phe 405	Asn	His	Gly	Ile	Cys 410	Asp	Trp	Lys	Gln	Asp	Arg 415
Glu	Asp	Asp	Phe 420	Asp	Trp	Asn	Pro	Ala 425	Asp	Arg	Asp	Asn	Ala	Ile	Gly
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Arg 450	Leu	Lys	Leu	Leu	Leu	Pro 455	Asp	Leu	Gln	Pro	Gln 460	Ser	Asn	Phe	Cys
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Val	Phe	Val	Lys 485	Asn	Ser	Asn	Asn	Ala	Leu 490	Ala	Trp	Glu	Lys	Thr	Thr 495
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agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac						578										
Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His																
		95		100		105										
aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc						626										
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly																
		110		115		120										
cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc						674										
His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala																
		125		130		135										
atg ata aac tgt cag tac agc tgt gaa gac aca gaa gaa ggg cca cag						722										
Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln																
		140		145		150		155								
tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac						770										
Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp																
		160		165		170										

tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac	818
Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr	
175 180 185	
aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac	866
Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His	
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Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp	
205 210 215	
ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat	962
Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn	
220 225 230 235	
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Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr	
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Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys	
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Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu	
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Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val	
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Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro	
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly	
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Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys	
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Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg	
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Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu	
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Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala	
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 Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His
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 Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro
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 Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys
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Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
35 40 45

Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
50 55 60

Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
65 70 75 80

Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
85 90 95

Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
100 105 110

His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
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Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
130 135 140

Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
145 150 155 160

Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
165 170 175

Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
210 215 220

Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn
275 280 285

Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
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09061649 101504

Ile	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe		
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Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg		
						370							380				
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Ala	Asp	Leu	Asn	Ile	Ser		
						390							395				
Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg		
						405							410				
Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly		
						420							425				
Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	Lys	Lys	Asp	Ile	Gly		
						435							440				
Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys		
						450							455				
Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg		
						465							470				
Val	Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr		
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Ser	Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly		
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Thr	Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly		
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Lys	Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu		
						530							535				
Cys	Pro	Asp	Ser	Leu	Leu	Ser	Val	Asp	Asp								
						545							550				